OIPE
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JC16
PATENT & TRADEMARK OFFICE

SEQUENCE LISTING

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TECH CENTER 1600/2900

<110> Monsanto Company

<120> TRANSGENIC PLANTS CONTAINING ALTERED LEVELS OF STEROL COMPOUNDS AND TOCOPHEROLS

<130> MTC 6462.1

<140> 09/548,256
<141> 2000-04-12

<150> 60/128,995
<151> 1999-04-12

<160> 31

<170> PatentIn Ver. 2.1

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Leu Pro Val Thr Pro Gly Ser Lys Asp Lys Pro Val Val Leu Asn Ser
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Lys Lys Ser Leu Lys Glu Tyr Cys Asp Gly Asn Asn Asn Ser Leu Thr
65 70 75 80

Val Val Phe Lys Asp Leu Gly Ala Gln Val Ser Tyr Arg Thr Leu Phe
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Phe Phe Glu Tyr Leu Gly Pro Leu Leu Ile Tyr Pro Val Phe Tyr Tyr
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Phe Pro Val Tyr Lys Phe Leu Gly Tyr Gly Glu Asp Cys Val Ile His
115 120 125

Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
130 135 140

Arg Ile Leu Glu Thr Phe Phe Val His Arg Phe Ser His Thr Ser Pro
145 150 155 160

Ile Gly Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Ser Phe Gly Ala
165 170 175

Tyr Ile Ala Tyr Tyr Val Asn His Pro Leu Tyr Thr Pro Val Ser Asp
180 185 190

Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Leu Val Cys Gln Val Ala
195 200 205

Asn Phe Tyr Cys His Ile Leu Leu Lys Asn Leu Arg Asp Pro Ser Gly
210 215 220

Ala Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr
225 230 235 240

Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Leu Gly Phe Asn Ile
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Ala Thr Gln Thr Ile Ala Gly Tyr Val Phe Leu Ala Val Ala Ala Leu
260 265 270

Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Arg Lys Ile
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Ile His Ala Arg Thr Lys Lys Tyr Tyr Pro Ser Arg Gln Arg Leu Thr
         35                  40                  45

Leu Pro Leu Gln Pro Gly Lys Gly Gly Lys Pro Val Val Leu Ser Pro
     50                  55                  60

Lys Ala Ser Leu Leu Glu Tyr Cys Glu Lys Gly Ser Gly Ser Leu Thr
 65                  70                  75                  80

Val Val Phe Lys Asp Leu Gly Pro Gln Val Tyr Tyr Ser Thr Leu Phe
                 85                  90                  95

Phe Phe Glu Tyr Leu Gly Pro Leu Ile Ile Tyr Pro Met Phe Tyr Tyr
            100                 105                 110

Leu Pro Val Tyr Lys Tyr Phe Gly His Glu Gly Glu Arg Ala Met His
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Pro Val Gln Thr Tyr Ala Met Tyr Tyr Trp Cys Phe His Tyr Phe Lys
130 135 140

Arg Ile Met Glu Thr Phe Phe Val His Arg Phe Ser Ala Thr Ser Pro
145 150 155 160

Leu Ser Asn Val Phe Arg Asn Cys Ala Tyr Tyr Trp Thr Phe Gly Ala
165 170 175

Tyr Ile Ala Tyr Tyr Cys Asn His Pro Leu Tyr Thr Pro Val Ser Asp
180 185 190

Leu Gln Met Lys Ile Gly Phe Gly Phe Gly Val Val Cys Gln Val Ala
195 200 205

Asn Phe Tyr Cys His Ile Leu Leu Arg Asn Leu Arg Ser Pro Ser Gly
210 215 220

Ser Gly Gly Tyr Gln Ile Pro Arg Gly Phe Leu Phe Asn Ile Val Thr
225 230 235 240

Cys Ala Asn Tyr Thr Thr Glu Ile Tyr Gln Trp Val Gly Phe Asn Ile
245 250 255

Ala Thr Gln Thr Val Ala Gly Tyr Val Phe Leu Val Val Ala Ala Gly
260 265 270

Ile Met Thr Asn Trp Ala Leu Gly Lys His Ser Arg Leu Lys Lys Leu
275 280 285

Phe Asp Gly Lys Asp Gly Arg Pro Lys Tyr Pro Arg Arg Trp Val Ile
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Leu Pro Pro Phe Leu
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             20                  25                  30

Ser Ala Glu Lys Gln Val Lys Leu Ser Ser Lys Ala Gly Met Leu Leu
         35                  40                  45

Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu Ala Ser Phe Trp Ile Phe
     50                  55                  60

Pro His Gln Gly Leu Arg Ser Thr Leu Leu Gln Ser Ala Val Thr Leu
 65                  70                  75                  80

His Phe Phe Lys Arg Val Phe Glu Val Val Phe Ile His Lys Tyr Ser
                 85                  90                  95

Gly Ala Met Leu Leu Asp Ser Ala Ile Pro Ile Thr Leu Ser Tyr Phe
            100                 105                 110

Leu Ser Thr Ala Thr Met Ile Tyr Ala Gln His Leu Thr Gln Gly Leu
        115                 120                 125

Pro Glu Pro Pro Ile Asp Leu Leu Tyr Pro Gly Ile Val Leu Phe Val
    130                 135                 140

Val Gly Ile Ile Gly Asn Phe Tyr His His Tyr Leu Leu Ser Asn Leu
145                 150                 155                 160
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Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile Pro Lys Gly Gly Met Phe
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Glu Leu Val Ile Cys Pro His Tyr Leu Phe Glu Ile Ile Glu Phe Tyr
180 185 190

Gly Phe Ser Phe Ile Ser Gln Thr Leu Tyr Ala Phe Ser Phe Thr Val
195 200 205

Gly Thr Thr Leu Tyr Leu Leu Gly Arg Ser Tyr Ser Thr Arg Lys Trp
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         35                  40                  45

Phe Trp Asn Ala Asn Pro Ser Ala Glu Lys Gln Val Lys Leu Ser Ser
     50                  55                  60

Lys Ala Gly Met Leu Leu Leu Tyr Thr Pro Ala Phe Leu Ala Gly Leu
 65                  70                  75                  80

Ala Ser Phe Trp Val Phe Pro His Gln Gly Leu Arg Phe Thr Ile Leu
                 85                  90                  95

Gln Ser Ala Val Thr Leu His Tyr Phe Lys Arg Val Phe Glu Gly Leu
            100                 105                 110

Phe Ile His Lys Tyr Ser Gly Gly Met Thr Leu Glu Ser Ala Ile Pro
        115                 120                 125

Ile Thr Leu Ser Tyr Phe Leu Ser Ala Val Thr Met Val Tyr Ser Gln
    130                 135                 140

His Leu Thr Lys Gly Phe Pro Glu Pro Pro Ile Asn Leu Phe Tyr Pro
145                 150                 155                 160

Gly Ile Val Leu Phe Leu Val Gly Ile Ile Gly Asn Phe Tyr His His
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Tyr Leu Leu Ser Lys Leu Arg Gly Lys Gly Glu Lys Glu Tyr Lys Ile
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Pro Lys Gly Gly Phe Phe Glu Leu Val Ile Cys Pro His Tyr Phe Phe
        195                 200                 205

Glu Ile Thr Val Phe Tyr Gly Ile Phe Phe Ile Ser Gln Thr Leu Tyr
    210                 215                 220

Ser Phe Ala Phe Ala Val Gly Thr Thr Met Tyr Leu Val Gly Arg Ser
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Tyr Ser Thr Arg Lys Trp Tyr Leu Ser Lys Phe Glu Asp Phe Pro Lys
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             20                  25                  30

Ser Asp Ser Ser Asn Gly Leu Leu Leu Ser Gly Ser Asp Asn Asn Ser
         35                  40                  45

Pro Ser Asp Asp Val Gly Ala Pro Ala Asp Val Arg Asp Arg Ile Asp
     50                  55                  60

Ser Val Val Asn Asp Asp Ala Gln Gly Thr Ala Asn Leu Ala Gly Asp
 65                  70                  75                  80

Asn Asn Gly Gly Gly Asp Asn Asn Gly Gly Gly Arg Gly Gly Gly Glu
                 85                  90                  95

Gly Arg Gly Asn Ala Asp Ala Thr Phe Thr Tyr Arg Pro Ser Val Pro
            100                 105                 110

Ala His Arg Arg Ala Arg Glu Ser Pro Leu Ser Ser Asp Ala Ile Phe
        115                 120                 125

Lys Gln Ser His Ala Gly Leu Phe Asn Leu Cys Val Val Val Leu Ile
    130                 135                 140

Ala Val Asn Ser Arg Leu Ile Ile Glu Asn Leu Met Lys Tyr Gly Trp
145                 150                 155                 160

Leu Ile Arg Thr Asp Phe Trp Phe Ser Ser Arg Ser Leu Arg Asp Trp
                165                 170                 175

Pro Leu Phe Met Cys Cys Ile Ser Leu Ser Ile Phe Pro Leu Ala Ala
            180                 185                 190

Phe Thr Val Glu Lys Leu Val Leu Gln Lys Tyr Ile Ser Glu Pro Val
        195                 200                 205

Val Ile Phe Leu His Ile Ile Ile Thr Met Thr Glu Val Leu Tyr Pro
    210                 215                 220

Val Tyr Val Thr Leu Arg Cys Asp Ser Ala Phe Leu Ser Gly Val Thr
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Leu Met Leu Leu Thr Cys Ile Val Trp Leu Lys Leu Val Ser Tyr Ala
245 250 255

His Thr Ser Tyr Asp Ile Arg Ser Leu Ala Asn Ala Ala Asp Lys Ala
260 265 270

Asn Pro Glu Val Ser Tyr Tyr Val Ser Leu Lys Ser Leu Ala Tyr Phe
275 280 285

Met Val Ala Pro Thr Leu Cys Tyr Gln Pro Ser Tyr Pro Arg Ser Ala
290 295 300

Cys Ile Arg Lys Gly Trp Val Ala Arg Gln Phe Ala Lys Leu Val Ile
305 310 315 320

Phe Thr Gly Phe Met Gly Phe Ile Ile Glu Gln Tyr Ile Asn Pro Ile
325 330 335

Val Arg Asn Ser Lys His Pro Leu Lys Gly Asp Leu Leu Tyr Ala Ile
340 345 350

Glu Arg Val Leu Lys Leu Ser Val Pro Asn Leu Tyr Val Trp Leu Cys
355 360 365

Met Phe Tyr Cys Phe Phe His Leu Trp Leu Asn Ile Leu Ala Glu Leu
370 375 380

Leu Cys Phe Gly Asp Arg Glu Phe Tyr Lys Asp Trp Trp Asn Ala Lys
385 390 395 400

Ser Val Gly Asp Tyr Trp Arg Met Trp Asn Met Pro Val His Lys Trp
405 410 415

Met Val Arg His Ile Tyr Phe Pro Cys Leu Arg Ser Lys Ile Pro Lys
420 425 430

Thr Leu Ala Ile Ile Ile Ala Phe Leu Val Ser Ala Val Phe His Glu
435 440 445

Leu Cys Ile Ala Val Pro Cys Arg Leu Phe Lys Leu Trp Ala Phe Leu
450 455 460

Gly Ile Met Phe Gln Val Pro Leu Val Phe Ile Thr Asn Tyr Leu Gln
465 470 475 480

Glu Arg Phe Gly Ser Thr Val Gly Asn Met Ile Phe Trp Phe Ile Phe

485 490 495

Cys Ile Phe Gly Gln Pro Met Cys Val Leu Leu Tyr Tyr His Asp Leu
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Met Asn Arg Lys Gly Ser Met Ser
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<213> Caenorhabditis elegans

<400> 14

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20 25 30

Asn Ser Ser Arg Lys Ser Ser Glu Met Arg Gly Pro Cys Glu Lys Val
35 40 45

Val His Thr Ala Gln Asp Ser Leu Phe Ser Thr Ser Ser Gly Trp Thr
50 55 60

Asn Phe Arg Gly Phe Phe Asn Leu Ser Ile Leu Leu Leu Val Leu Ser
65 70 75 80

Asn Gly Arg Val Ala Leu Glu Asn Val Ile Lys Tyr Gly Ile Leu Ile
85 90 95

Thr Pro Leu Gln Trp Ile Ser Thr Phe Val Glu His His Tyr Ser Ile
100 105 110

Trp Ser Trp Pro Asn Leu Ala Leu Ile Leu Cys Ser Asn Ile Gln Ile
115 120 125

Leu Ser Val Phe Gly Met Glu Lys Ile Leu Glu Arg Gly Trp Leu Gly
130 135 140

Asn Gly Phe Ala Ala Val Phe Tyr Thr Ser Leu Val Ile Ala His Leu
145 150 155 160

Thr Ile Pro Val Val Val Thr Leu Thr His Lys Trp Lys Asn Pro Leu
165 170 175

Trp Ser Val Val Met Met Gly Val Tyr Val Ile Glu Ala Leu Lys Phe
180 185 190

Ile Ser Tyr Gly His Val Asn Tyr Trp Ala Arg Asp Ala Arg Arg Lys
195 200 205

Ile Thr Glu Leu Lys Thr Gln Val Thr Asp Leu Ala Lys Lys Thr Cys
210 215 220

Asp Pro Lys Gln Phe Trp Asp Leu Lys Asp Glu Leu Ser Met His Gln
225 230 235 240

Met Ala Ala Gln Tyr Pro Ala Asn Leu Thr Leu Ser Asn Ile Tyr Tyr
245 250 255

Phe Met Ala Ala Pro Thr Leu Cys Tyr Glu Phe Lys Phe Pro Arg Leu
260 265 270

Leu Arg Ile Arg Lys His Phe Leu Ile Lys Arg Thr Val Glu Leu Ile
275 280 285

Phe Leu Ser Phe Leu Ile Ala Ala Leu Val Gln Gln Trp Val Val Pro
290 295 300

Thr Val Arg Asn Ser Met Lys Pro Leu Ser Glu Met Glu Tyr Ser Arg
305 310 315 320

Cys Leu Glu Arg Leu Leu Lys Leu Ala Ile Pro Asn His Leu Ile Trp
325 330 335

Leu Leu Phe Phe Tyr Thr Phe Phe His Ser Phe Leu Asn Leu Ile Ala
340 345 350

Glu Leu Leu Arg Phe Ala Asp Arg Glu Phe Tyr Arg Asp Phe Trp Asn
355 360 365

Ala Glu Thr Ile Gly Tyr Phe Trp Lys Ser Trp Asn Ile Pro Val His
370 375 380

Arg Phe Ala Val Arg His Ile Tyr Ser Pro Met Met Arg Asn Asn Phe
385 390 395 400

Ser Lys Met Ser Ala Phe Phe Val Val Phe Phe Val Ser Ala Phe Phe
405 410 415

His Glu Tyr Leu Val Ser Val Pro Leu Lys Ile Phe Arg Leu Trp Ser
420 425 430

Tyr Tyr Gly Met Met Gly Gln Ile Pro Leu Ser Ile Ile Thr Asp Lys
435 440 445

Val Val Arg Gly Gly Arg Thr Gly Asn Ile Ile Val Trp Leu Ser Leu
450 455 460

Ile Val Gly Gln Pro Leu Ala Ile Leu Met Tyr Gly His Asp Trp Tyr
465 470 475 480

Ile Leu Asn Phe Gly Val Ser Ala Val Gln Asn Gln Thr Val Gly Ile
485 490 495

<210> 15
<211> 257
<212> DNA
<213> Glycine max

<400> 15
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ggcttttgga aaaactggca tgcttccttc aacaagtggc ttgtgaggta tatatacatt 120
cctcttgggg gatctaagaa aaagctacta aatgtgtggg ttgttttcac atttgttgca 180
atctggcatg atttagagtg gaagcttctt tcatgggcat ggttgacgtg tttattcttc 240
atccctgagt tggtttt 257

<210> 16
<211> 234
<212> DNA
<213> Glycine max

<220>
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<222> (24)
<223> n=a, t, c or g

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<222> (41)
<223> n=a, t, c or g

<220>
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<222> (60)
<223> n=a, t, c or g

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atatttacag gagttatggg atttataata gaacaataca ttaatcccat tgtacaaaat 180
tcacagcatc ctctcaaggg aaaccttctt tacgccatcg agagagttct gaag 234

<210> 17
<211> 275
<212> DNA
<213> Glycine max

<220>
<221> unsure

<222> (192)
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<222> (234)
<223> n=a, t, c or g

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<222> (238)..(239)
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<220>
<221> unsure
<222> (244)..(245)
<223> n=a, t, c or g

<220>
<221> unsure
<222> (251)
<223> n=a, t, c or g

<220>
<221> unsure
<222> (262)..(263)
<223> n=a, t, c or g

<400> 17
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gatgatccgc cacctatatt ttccatgttt aaggcacggt ataccaaagg ccgttgctct 120
tttaattgcc ttcctggttc tgctttattc catgagctgt gcatcgctgt tccttgccca 180
catattcaag tngtgggttt cngnggaatt nagtttcagg tnccttgggt ttcnaccnna 240
attnntnggc naaaaaattc cnngaacccc ggggg 275

<210> 18
<211> 267
<212> DNA
<213> Glycine max

<400> 18
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tgtcatatgc acatacaaac tatgatatga gagcacttac tgtttcgaat gaaaagggag 120
aaacattacc caatactttg atatggagta tccgtacact gtgaccttca ggagtttggc 180
atacttcatg gttgctccta cattatgcta tcagacaagc tatcctcgca caccttcagt 240
tcgaaagggt tgggtgtttc gtcaact 267

<210> 19
<211> 1895
<212> DNA
<213> Human

<220>
<221> unsure
<222> (209)
<223> n=a, t, c or g

<400> 19
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ggctgccgcc ctgagctcgg gctgggacgt gcccagaggt gttgggagga tctggggtga 180
gtaccctgtg gccaggacta aaggggctnc accctcctgt ccatccctcg cagatcttga 240
gcaatgcccg gttatttctg gagaacctca tcaagtatgg catcctggtg gaccccatcc 300
aggtggtttc tctgttcctg aaggatccct atagctggcc cgccccatgc ctggttattg 360
cggccaatgt ctttgctgtg gctgcattcc aggttgagaa gcgcctggcg gtgggtgccc 420
tgacggagca ggcgggactg ctgctgcacg tggccaacct ggccaccatt ctgtgtttcc 480
cagcggctgt ggtcttactg gttgagtcta tcactccagt gggctccctg ctggcgctga 540
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gcagggccag ggccaaggct gcctctgcag ggaagaaggc cagcagtgct gctgccccgc 660
acaccgtgag ctacccggac aatctgacct accgcgatct ctactacttc ctcttcgccc 720
ccaccttgtg ctacgagctc aactttcccc gctctccccg catccggaag cgctttctgc 780
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cccctaccta gaaaagctca gctcaggcgt cctct 1895

<210> 20
<211> 519
<212> DNA
<213> Montierella alphina

<220>
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<222> (4)..(7)
<223> n=a, t, c or g

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<223> n=a, t, c or g

<220>
<221> unsure
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<223> n=a, t, c or g

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<223> n=a, t, c or g

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aacggagcac tatatttacc ccgtggtngt tcaacccagc catctcaccc ttgcgagcat 180
tggtgctgct cttgataccc ttcatgctta actatctcat gatcttttac atcattttcg 240
agtgcatctg caacgccttt gcggaactaa gttgctttgc ggatcgcaac ttttacgagg 300
attggtggaa ctgcgtcagc tttgatgagt gggcacgcaa atggaacaag cctgtgcaac 360
acttcttgct ccgccacgtg tacgactcga gcatccgagt ccttccactt gtccgaaatc 420
caatgccgcn aattgcaaac gttccttccc ggtcgtcaat gcgttcaacg aacctgggtg 480
aagaatgggt ggtgacaacg ttaaagtgcg cccggtatc 519

<210> 21
<211> 518
<212> DNA
<213> mouse

<400> 21
tggaggacaa cgcggggtct gatacgactc actataggga atttggccct cgagcagtag 60
attcggcacg atgggcacga ggactccatc atgttcctca agctttattc ctaccgggat 120
gtcaacctgt ggtgccgcca gcgaagggtc aaggccaaag ctgtctctac agggaagaag 180
gtcagtgggg ctgctgcgag caagctgtga gctatccaga caacctgacc taccgagatc 240
tcgattactt catctttgct cctactttgt gttatgaact caactttcct cggtcccccc 300
gaatacgaga gcgctttctg ctacgacgag ttcttgagat gctctttttt acccagcttc 360
aagtggggct gatccaacag tggatggtcc ctactatcca gaactccatg gaagcccttt 420
caagagcttc tgcagttttg gagaccgcga gttctacaga gattggtgga atgctgagtc 480
tgtcaccgac ttttggcaga actggaatat ccccgtgg 518

<210> 22
<211> 299
<212> DNA
<213> mouse

<400> 22
ccatgatggc tcaggtccca ctggcctgga ttgtgggccg attcttccaa gggaactatg 60
gcaatgcagc tgtgtgggtg acactcatca ttgggcaacc ggtggctgtc tcatgtatgt 120
ccacgactac tacgtgctca actacgatgc cccagtgggt catgagctac tgccaaaggc 180
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<210> 23
<211> 1766
<212> DNA
<213> Rat

<400> 23
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gccgccagcg aagggtcaag gccaaagctg tgtctgcagg gaagaaggtc agtggggctg 780
ctgcccagaa cactgtaagc tatccggaca acctgaccta ccgagatctc tattacttca 840
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<210> 24
<211> 500
<212> PRT
<213> rat

<400> 24
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Ser Arg Val Ser Ile Gln Gly Gly Ser Gly Pro Met Val Asp Glu Glu
20 25 30

Glu Val Arg Asp Ala Ala Val Gly Pro Asp Leu Gly Ala Gly Gly Asp
35 40 45

Ala Pro Ala Pro Ala Pro Val Pro Ala Pro Ala His Thr Arg Asp Lys
50 55 60

Asp Arg Gln Thr Ser Val Gly Asp Gly His Trp Glu Leu Arg Cys His
65 70 75 80

Arg Leu Gln Asp Ser Leu Phe Ser Ser Asp Ser Gly Phe Ser Asn Tyr
85 90 95

Arg Gly Ile Leu Asn Trp Cys Val Val Met Leu Ile Leu Ser Asn Ala
100 105 110

Arg Leu Phe Leu Glu Asn Leu Ile Lys Tyr Gly Ile Leu Val Asp Pro
115 120 125

Ile Gln Val Val Ser Leu Phe Leu Lys Asp Pro Tyr Ser Trp Pro Ala
130 135 140

Pro Cys Leu Ile Ile Ala Ser Asn Ile Phe Ile Val Ala Thr Phe Gln
145 150 155 160

Ile Glu Lys Arg Leu Ser Val Gly Ala Leu Thr Glu Gln Met Gly Leu
165 170 175

Leu Leu His Val Val Asn Leu Ala Thr Ile Ile Cys Phe Pro Ala Ala
180 185 190

Val Ala Leu Leu Val Glu Ser Ile Thr Pro Val Gly Ser Leu Phe Ala
195 200 205

Leu Ala Ser Tyr Ser Ile Ile Phe Leu Lys Leu Phe Ser Tyr Arg Asp
210 215 220

Val Asn Leu Trp Cys Arg Gln Arg Arg Val Lys Ala Lys Ala Val Ser
225 230 235 240

Ala Gly Lys Lys Val Ser Gly Ala Ala Ala Gln Asn Thr Val Ser Tyr
245 250 255

Pro Asp Asn Leu Thr Tyr Arg Asp Leu Tyr Tyr Phe Ile Phe Ala Pro
260 265 270

Thr Leu Cys Tyr Glu Leu Asn Phe Pro Arg Ser Pro Arg Ile Arg Lys
275 280 285

Arg Phe Leu Leu Arg Arg Val Leu Glu Met Leu Phe Phe Thr Gln Leu
290 295 300

Gln Val Gly Leu Ile Gln Gln Trp Met Val Pro Thr Ile Gln Asn Ser
305 310 315 320

Met Lys Pro Phe Lys Asp Met Asp Tyr Ser Arg Ile Ile Glu Arg Leu
325 330 335

Leu Lys Leu Ala Val Pro Asn His Leu Ile Trp Leu Ile Phe Phe Tyr
340 345 350

Trp Leu Phe His Ser Cys Leu Asn Ala Val Ala Glu Leu Leu Gln Phe
355 360 365

Gly Asp Arg Glu Phe Tyr Arg Asp Trp Trp Asn Ala Glu Ser Val Thr
370 375 380

Tyr Phe Trp Gln Asn Trp Asn Ile Pro Val His Lys Trp Cys Ile Arg
385 390 395 400

His Phe Tyr Lys Pro Met Leu Arg Leu Gly Ser Asn Lys Trp Met Ala
405 410 415

Arg Thr Gly Val Phe Leu Ala Ser Ala Phe Phe His Glu Tyr Leu Val
420 425 430

Ser Ile Pro Leu Arg Met Phe Arg Leu Trp Ala Phe Thr Ala Met Met
435 440 445

Ala Gln Val Pro Leu Ala Trp Ile Val Asn Arg Phe Phe Gln Gly Asn
450 455 460

Tyr Gly Asn Ala Ala Val Trp Val Thr Leu Ile Ile Gly Gln Pro Val
465 470 475 480

Ala Val Leu Met Tyr Val His Asp Tyr Tyr Val Leu Asn Tyr Asp Ala
485 490 495

Pro Val Gly Ala
500

<210> 25
<211> 325

<212> DNA
<213> Zea mays

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<222> (6)
<223> n=a, t, c or g

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<222> (317)
<223> n=a, t, c or g

<220>
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<222> (321)
<223> n=a, t, c or g

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cacatantca natctnggca tnncngggat catngttcag ataccgntgg nattcttgac 120
aagatatctc catgctacgt tcaagcatgt aatggtgggc aacatgatan tttggntctn 180
cagtatagtc ggacagccga tgtnnnnnna tctatactac catgacgtca tgaacaggca 240
ggcccaggca agtagatagt ncggcagaga catgtacttc aacatcganc atcagnagca 300
nacngagcga gcggcangaa ncagc 325

<210> 26
<211> 262
<212> DNA
<213> Zea mays

<400> 26
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aaagttggca ttcaacaatc tcattagtga tcctgctact acctgttttc acatcctttt 180
tacaacattt gaaattgtat atccagtgct cgtgattctt aagtgtgatt ctgcagtttt 240
acaggctttg tgttgatgtt ta 262

<210> 27
<211> 253
<212> DNA
<213> Zea mays

<400> 27
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atgagttatg tgttgctgtt ccctgccaca tactcaagtt ctgggctttt tttaggaatc 180
atgcttcaga ttcccctcat catattgaca tcatacctca aaaataaatt cagtgacaca 240
atggttggca ata 253

<210> 28
<211> 254
<212> DNA
<213> Zea mays

<400> 28
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Met Asp Asn Cys Lys Pro Cys Gly Gly Ala Ile Pro Leu Cys Met Val
         35                  40                  45

Ser Glu Phe Asp Leu Pro Leu Asp Leu Val Asp Arg Lys Val Arg Lys
     50                  55                  60

Met Lys Met Ile Ser Pro Ser Asn Val Ala Val Asp Ile Gly Arg Thr
 65                  70                  75                  80

Leu Ala Pro His Glu Tyr Ile Gly Met Val Arg Arg Glu Val Leu Asp
                 85                  90                  95

Ala Tyr Leu Arg Ser Arg Ala Gln Ser Val Gly Ala Glu Val Val Asn
            100                 105                 110

Gly Leu Phe Leu Arg Tyr Glu Ala Pro Lys Glu Pro Asn Gly Ser Tyr
        115                 120                 125

Val Val His Tyr Asn His Tyr Asp Gly Ser Asn Gly Lys Val Gly Gly
    130                 135                 140

Glu Lys Arg Ser Phe Glu Val Asp Ala Ile Val Gly Ala Asp Gly Ala
145                 150                 155                 160

Asn Ser Arg Val Ala Asn Asp Met Gly Ala Gly Asp Tyr Glu Tyr Ala
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Ile Ala Phe Gln Glu Arg Val Lys Ile Pro Asp Asp Lys Met Val Tyr
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Tyr Glu Glu Arg Ala Glu Met Tyr Val Gly Asp Asp Val Ser Pro Asp
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Phe Tyr Gly Trp Val Phe Pro Lys Cys Asp His Val Ala Val Gly Thr
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[redacted] [redacted]

210 215 220

Gly Thr Val Thr His Lys Ala Asp Ile Lys Lys Phe Gln Ala Ala Thr
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245 250 255

Glu Ala His Pro Ile Pro Glu His Pro Arg Pro Lys Arg Val Ser Gly
260 265 270

Arg Val Thr Leu Val Gly Asp Ala Ala Gly Tyr Val Thr Lys Cys Ser
275 280 285

Gly Glu Gly Ile Tyr Phe Ala Ala Lys Ser Gly Arg Met Cys Ala Glu
290 295 300

Ala Ile Val Ala Gly Ser Ala Asn Gly Thr Arg Met Val Glu Glu Ser
305 310 315 320

Asp Leu Arg Lys Tyr Leu Ala Glu Phe Asp Arg Leu Tyr Trp Pro Thr
325 330 335

Tyr Lys Val Leu Asp Ile Leu Gln Lys Val Phe Tyr Arg Ser Asn Ala
340 345 350

Ala Arg Glu Ala Phe Val Glu Met Cys Ala Asp Asp Tyr Val Gln Lys
355 360 365

Met Thr Phe Asp Ser Tyr Leu Tyr Lys Arg Val Val Pro Gly Asn Pro
370 375 380

Leu Asp Asp Ile Lys Leu Ala Val Asn Thr Ile Gly Ser Leu Val Arg
385 390 395 400

Ala Thr Ala Leu Arg Arg Glu Met Glu Lys Val Thr Leu Xaa Ala Ala
405 410 415

Ala Arg Asp Val Ile Ala Val Glu Met Val Ser Gln Leu Ile Gly Arg
420 425 430

Cys Ile Ser Arg Asp Leu Arg Leu Ile Gly Leu Ile Xaa Ala Asn Met
435 440 445

Arg Gly Gln Trp Ala Arg Arg Gly Arg Glu Thr Ser Cys Ala Ser Ala
450 455 460

Ala Ser Arg Ser Lys Val Leu Pro Val Cys Ile Asp Gly Ser Cys Asn

465 470 475 480

Ile Xaa His Leu Val Met Leu Arg Ile Arg Ser Ser Ser Ser Thr Gly
485 490 495

Phe Xaa Arg Arg Gln Ala Ser Thr Ser Met Asn Val Xaa Tyr Leu Val
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His Gln Asp Met Xaa Xaa Asn Xaa Asn Ser Pro Val Leu Val Gln Lys
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Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Gly Arg
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<212> PRT
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Gly Phe Pro Phe Thr Gly Leu Lys Ser Met Ala Gly Phe Pro Thr Arg
35 40 45

Lys Thr Asn Asn Asp Ile Thr Ser Ile Ala Ser Asn Gly Gly Arg Val
50 55 60

Gln Cys Met Gln Val Trp Pro Pro Ile Gly Lys Lys Lys Phe Glu Thr
65 70 75 80